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Result
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Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Post-processing: Minimum Match 0%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Total number of hits satisfying chosen parameters:
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120
121
121
                                                                                                                                                                                                                                                                                                                                           Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
 3326
3227
3215
1116
1092.5
1015
888
864.5
863.5
863.5
861
                                                                                                                                                                                                                                                  Score
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   protein search, using sw model
                                                                                                                                                                                                                                                Match Length DB
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Query
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96
96
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26
25
                                                                                                                                                                                                                                                                                                                                                                                                              | SIDS1/gcgdata/geneseq/geneseqp/AA1980.DAT: *
| SIDS1/gcgdata/geneseq/geneseqp/AA1981.DAT: *
| SIDS1/gcgdata/geneseq/geneseqp/AA1982.DAT: *
| SIDS1/gcgdata/geneseq/geneseqp/AA1983.DAT: *
| SIDS1/gcgdata/geneseq/geneseqp/AA1985.DAT: *
| SIDS1/gcgdata/geneseq/geneseqp/AA1985.DAT: *
| SIDS1/gcgdata/geneseq/geneseqp/AA1985.DAT: *
| SIDS1/gcgdata/geneseq/geneseqp/AA1987.DAT: *
| SIDS1/gcgdata/geneseq/geneseqp/AA1987.DAT: *
| SIDS1/gcgdata/geneseq/geneseqp/AA1987.DAT: *
| SIDS1/gcgdata/geneseq/geneseqp/AA1997.DAT: *
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3326
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A_Geneseq_36:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gapop 10.0 , Gapext 0.5
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Copyright (c) 1993 - 2000 Compugen Ltd
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                 W62830
W62829
W62829
R20181
W62832
W62831
W62835
W62837
Y15244
Y25657
                                                                                                                                                                                                                                                                                                         SUMMARIES
               Gossypium hirsutum
Theobroma cacao an
Zea mays antimicro
Hordeum vulgare an
Peanut allergen, A
Peanut allergen 11
Peanut allergen Ar
                                                                                                                                                                                                                                              Description
                                                                                                                                                Sequence encoded b
                                                                                                                                                                 Macadamia integrif
Macadamia integrif
Macadamia integrif
Arachis hypogaea
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Full length human	Y55966	20	968	4.3	142	5
ıd	R60126	15	1805	4.3	143.5	44
estin	R27204	13	1805	4.3	143.5	ū
Human ZC2 protein.	Y55932	20	1297	4.4	146.5	12
Human CDC28-#3 RNA	W30613	20	1041	4.4	148	÷
cyt	Y91958	21	281	4.4	148	0
Human 2C3 protein.	Y55933	20	1326		158.5	39
Protein regulating	Y58633	21	1299	4.8	161	8
P.falciparum LSA-R	R26941	13	316		161.5	37
o.	R26944		493		163	36
	Y68784		1135		164	5
	Y55954		1233		165.5	34
Human thyrotropin	W03626		412		169	ü
follicle st	W03627		360		1.69	2
lobin	R47128		515	5.1	169.5	3
Human ZC1 protein.	Y55931		1239	5.2	174.5	30
3 allergen	Y40912		512	5.3	176	9
Peanut allergen, A	Y15246		510		177	8
	R70491		562		185.5	27
Rice storage prote	P82755		499		186.5	26
Modified oat globi	R47127		472		189	25
T. qondii immunoqe	Y29039		611	6.0	199	24
HHV8 ORF 73 protei	Y58500		1162		199.5	23
A human trichohyal	Y30795	20	1898		216	22
aseolin A chain	Y40914	20	371	5	526.5	21
ст.	W90342	20	409	0	677.5	20
ra h 1 allergen	Y40913	20	415	٢	724.5	19
trunc	W90340	20	444	2	743	8
. max SBP2	W90341	20	489	ω.	776.5	17
S	W90339	20	524	ω.	794	16
n beta-co	Y40999	20	605	5	842.5	5
aller	W22150	18	626		857.5	14
Glycine max antimi	W62838	19	605	5	59.	13

## ALIGNMENTS

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RESULT
WPI; 1998-377279/32.
N-PSDB; V42316.
                                                                                                02-JUL-1998.
                                                                                                                                             Protein
                                                                                                                                                                       Key
                                                                                                                                                                                       Macadamia integrifolia.
                          Bower NI, Goulter KC,
                                                                                                                  WO9827805-A1.
                                                                                                                                                                                                         antimicrobial protein; infestation; control
                                                                                                                                                                                                                          Macadamia integrifolia antimicrobial protein
                                                                                                                                                                                                                                          27-OCT-1998 (first entry)
                                                                                                                                                                                                                                                              W62830;
                                                                                                                                                                                                                                                                             W62830 standard; Protein; 625 AA
                                           (RETR-) COOP RES CENT TROPICAL PLANT PATHOLOGY
                                                             20-DEC-1996;
                                                                              22-DEC-1997;
                                                                                                                                                              Peptide
                                                             96AU-0004275
                                                                              97WO-AU00874
                                                                                                                                 /note= "signal peptide"
29..666
/note= "mature protein"
                                                                                                                                                                     Location/Qualifiers
                         Green JL,
                          Manners JM,
                         Marcus JP;
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Marcus

JР

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RESULT
W62828
ID W6
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AC W7
AC W
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Best Local
Matches 62
                                          antimicrobial
                                                                                                                   Macadamia integrifolia antimicrobial protein
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                                                                                                                                                                                           27-OCT-1998
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
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Pred. No. 1.3e-296;
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Pred. No. 1.7e-287;
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                                                                                           cqrrckeiceeeeeynrqrdpqqqyeqcqercqrheteprhmqtcqqrcerryekekrkq
                                                                                                                                                                                                                                                                                      604;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Page 39-41; 96pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Goulter KC,
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29..666
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96.6%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          English
                                                                                                                                                                                                                                                                            Score 3215; DB 17;
Pred. No. 2.1e-286;
""cmatches 14;
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The inventors claim a 67 kD and 31 kD T. cacao protein, and fragments, and encoding DNAs. The 47 kD and 31 kD proteins derived from the 67 kD precursor. T. cacao protein cDNA wa
                                            Claim 4; Fig
                                                                  expression
                                                                           Recombinant cocoa proteins - are responsible for flavour in cocoa beans and produced in large quantities using yeast and bacterial
                                                                                                                                             Spencer
                                                                                                                                                                                                              07-JUN-1991;
                                                                                                                                                                                                                                                                                Theobroma cacao
                                                                                                                                                                                                                                                                                                                        Sequence encoded by 67 kD
                                                                                                                                                                                                                                                                                                                                                                                            R20181 standard;
                                                                                                                                                                  (MRSC ) MARS
                                                                                                                                                                                        11-JUN-1990;
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                                                                                                                                                                                                                                                                                                    Cocoa; flavour;
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DB; Q20377.
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                                 22-DEC-1997;
                                                                                           02-JUL-1998
                                                                                                                                                     WO9827805-A1
                                                                                                                                                                                                            Gossypium hirsutum.
                                                                                                                                                                                                                                                                   antimicrobial protein;
                                                                                                                                                                                                                                                                                                                             Gossypium hirsutum antimicrobial protein.
                                                                                                                                                                                                                                                                                                                                                                                      27-OCT-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       W62832 standard;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           antimicrobial protein; infestation; control.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                22 lcsgvsaygrkqyerdprqqyeqcqrrceseateereqeqceqrcer-----ey 70
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                                                                                                                                                                                                                                                                                                                           inlisqspvysngngrffeacpedfsqfqnmdvavsafklnggaifvphynskatfvvfv
                                                                                                                                                                                                                                                                                      LRALKNYRLVLLEANPNAFVLPTHLDADAILLVIGGRGALKMIHRDNRESYNLECGDVIR 301
                                                                                                                                                                                                                                                                                                                                                                                      keqqrqqeeel-----grgyqqcqgrcqeqqqqqreqqqcqrkcweqykeq 116
                                                                                                                                                                                                                                                                                                                                                                                                          EEQQREDEEKYEERMKEGDNKRDPQQREYEDCRRHCEQQE--PRLQYQCQRRCQEQQRQH 182 :|||| | | | | | | | | | | ::
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ICEEEEEYNR---QRDPQQQYEQCQKRCQRRETEPRHMQICQQRCERRYEKEKRKQQKRY 124
 GHPVVFVSSGNENLLLFAFGINAQNNHENFLAGR 559
                             \verb|tdgygyaqmacphlsrqsqgsqsgrqdrreq| eeeseeetfgefqqvkaplspgdvfvapa|
                                               ASGEADVEMACPHLSGRHGGRGGGK--RHEEEEEEV-----HYEOVRARLSKREAIVVLA
                                                                                                                     YNLFNKRPLYSNKYGQAYEVKPEDYRQLQDMDVSVFIANITQGSMMGPFFNTRSTKVVVV 473
                                                                                                                                              ntqrekleeileeqrgqkrqqgqggmfrkakpeqiraisqqatspr----hrgge--rla
                                                                                                                                                                NTQTERLRGVLGQQR------EGVIIRASQEQIRELTRDDSESRRWHIRRGGESSRGP 413
                                                                                                                                                                                                        vpagstvyvvsqdnqekltiavlalpvnspgkyelffpagnnkpesyygafsyevletvf 295
                                                                                                                                                                                                                                      IPAGTTFYLINRDNNERLHIAKFLQTISTPGQYKEFFPAGGQNPEPYLSTFSKEILEAAL 361
                                                                                                                                                                                                                                                                     lkgindyrlamfeanpntfilphhcdaeaiyfvtngkgtitfvthenkesynvqrgtvvs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Goulter KC, Green JL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       525
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           30.5%; score 1015; DB 19; ilarity 41.1%; Pred. No. 1.2e-84; Conservative 91; Mismatches 158;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         96AU-0004275
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plants or mar
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Qy

QΥ DЬ Q DЬ Qy DЬ γQ DЬ δõ Db Qy DЬ δÃ рь QУ В

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Query Match
Best Local Similarity
Matches 208; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The sequence is that of an antimicrobial protein which can be used to control microbial infestations in plants and man
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 1; Page 58-60; 96pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Novel anti-microbial protein from e.g. Macadamia integrifolia \boldsymbol{\cdot} useful for controlling microbial infestations of plants or mammals
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 1998-377279/32.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        W62835;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bower NI, Goulter KC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          20-DEC-1996;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (RETR-) COOP RES CENT TROPICAL PLANT PATHOLOGY
    426
                                 261 lfgrhgqdkgiivrateeqtrelrrhasegghgphwplppfge-srgpyslldqrpsian
                                                              371 VLGQ--QREGVIIRASQEQIRELTRDDSE---SRRWHIRRGGESSRGPYNLFNKRPLYSN 425
                                                                                                                                                311 INRDNNERLHIAKFLQTISTPGQYKEFFPAGGQNPEPYLSTFSKEILEAALNTQTERLRG 370
                                                                                                                                                                                                                   141
                                                                                                                                                                                                                                       251 VLLEANPNAFVLPTHLDADAILLVIGGRGALKMIHRDNRESYNLECGDVIRIPAGTTFYL 310
                                                                                                                                                                                                                                                                                                                                                192
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                                                                                                                          antdgrkkivitkilhtisvpgefqfffgpggrnpesfissfsksigraayktssdrler 260
KYGQAYEVKPEDYRQLQDMDVSVFIANITQGSMMGPFFNTRSTKVVVVASGEADVEMACP 485
                                                                                                                                                                                                            avleanprsfvvpshtdahcicyvaegegvvttiengerrsytikqghvfvapagavtyl 200
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                                                                                                                                                                                                                                                                                                                          QRGGSGRYEEGEEKQSD-NPYYFDERSLSTRFRTEEGHISVLENFYGRSKLLRALKNYRL 250
                                                                                                                                                                                                                                                                                                                                                                                                                   EEKYEERMKEGDNKRDPQQREYEDCRRHCEQQEPRLQYQCQRRCQEQQRQHGRGGDLMNP 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      eddnhhhhgghksgqcvrrcedr---pwhqrprcleqc-reeerekrqersrheaddrsg 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EEYNRQRDPQQQYEQCOKRCQRRETEPRHMQ-ICQQRCERRYEKEKRKQQKRYEEQQRED 131
                                                                                                                                                                                                                                                                                                 ------kekqkdrrpyvfdrrsfrrvvrseqgslrvlrpfdevsrllrgirdyrv 140
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       protein; infestation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        96AU-0004275
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             26.7%; Score 888; DB 19; 36.7%; Pred. No. 6.4e-73; tive 87; Mismatches 181;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Green JL,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               181;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 593;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
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RESULT
W62837
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                      Claim 1; Page 60-62; 96pp; English
                                                                                                                                                                                                                                                                                                                                                                                                  Novel anti-microbial protein from e.g. Macadamia integrifolia useful for controlling microbial infestations of plants or mammals \ensuremath{\mathsf{N}}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bower NI,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       20-DEC-1996;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hordeum vulgare antimicrobial protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (RETR-) COOP RES CENT TROPICAL PLANT PATHOLOGY
203 E--EKQSDN--PYYFDERSLSTRFRTEEGHISVLENFYGRSKLLRALKNYRLVLLEANPN 258
                             120
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                                                                                        72
                                                                                                                   87
                                                                                                                                                 27
                                                                                                                                                               Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           | dhgqlycadarsfhdlachdvsvsfanitagsmsaplfntrsfkiayvpngkgyaeivcp
                                            DPQQREYEDCRRHCEQQEPRLQYQCQRRCQEQQRQHGRG----GDLMNPQRGGGGRYEEG 202
                                                                                                                  QCQKRCQRRETEPRHMQICQQRCERRYEKEKRKQQKRYEEQQREDEEKYEERMKEGDNKR 146
                                                                                                                                            ashddeddrrgghslqqcvqrcrqer--pr---ysharcvqec-----rddqqqh- 71
                          gegereeergrghgrhgege-----reeergrgrgrhgegereeeegrgrgrrgeg 170
                                                                                   -----grheqeeeqgrgrgwhgegereeehgrgrgrhgegereeehgrgrgrh 119
                                                                                                                                                                                                             221;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ekgflpgpeesggheeregeeeeree 524
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ESIFFPGPRQ---HQQQSPRSTKQQQ 614
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       hrqsqggesererdkgrrseeeeeesseeqeeagqgyhtirarlspgtafvvpaghpfva
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VSSGNENLLLFAFGINAQNNHENFLAGRERNVLQQIEPQAMELAFAASRKEVEELFNSQD 591
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Goulter KC,
                                                                                                                                                                                                                                                                                    637
                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     96AU-0004275.
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                                                                                                                                                                                                          26.0%; Score 864.5; DB 19; 35.0%; Pred. No. 1e-70; tive 100; Mismatches 219;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Green JL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            637
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Manners JM,
                                                                                                                                                                                                        219; Indels 91; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Marcus
                                                                                                                                                                                                                                    Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             JP;
                                                                                                                                                                                                                                                                                                                            mammalian
                                                                                                                                                                                                                                       637;
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                                                                                                                                                          (SOSI/)
(UYAR-)
(UYNY)
                                                                                                                                                                                                                     27-AUG-1998;
31-JAN-1998;
13-FEB-1998;
13-FEB-1998;
13-FEB-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                              allergy; immune response; transgenic; allergen; epitope;
immunoglobulin E; Ig E; binding site; peanut.
            Disclosure; Page 35-37; 46pp; English
                                        allergies
                                                    Modified allergen with reduced
                                                                                      N-PSDB; Z06382
                                                                                                  WPI; 1999-479189/40
                                                                                                                              Bannon GA,
                                                                                                                                                                                                                                                                                                                29-JAN-1999;
                                                                                                                                                                                                                                                                                                                                          05-AUG-1999
                                                                                                                                                                                                                                                                                                                                                                       W09938978-A1.
                                                                                                                                                                                                                                                                                                                                                                                                Arachis hypogea
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Peanut allergen, Ara h 1,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        09-NOV-1999 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Y15244 standard; Protein;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             376 ---REGVIIRASQEQIRELTRDDSE---SRRWHIRRGGESSRGPYNLFNKRPLYSNKYGQ 429
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      319 LHIAKFLQTISTPGQYKEFFPAGGQNPEPYLSTFSKEILEAALNTQTERLRGYLGQQ--- 375
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   231
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                                                                                                                                                             UNIV ARKANSAS.
UNIV NEW YORK
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98US-0073283.
98US-0074590.
98US-0074624.
98US-0074633.
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                                                                                                                                                             MT SINAI SCHOOL MEDICINE
                                                                                                                                Sampson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         amino acid sequence
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                                                      IgE binding, useful for treating e.g.
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Best Local Similarity
 Major histocompatibility complex; cl
allergen; grass; tree; weed; pollen;
                                                Peanut allergen 1168391 Ara h I protein fragment.
                                                                                    30-SEP-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        By modifying the IgE binding sites the ability of the allergen to provoke an immune response is downregulated. The epitopes of the IgE binding sites can therefore be modified in genetically engineered plants
                                                                                                                                                    Y25657 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This is the amino acid sequence of the Ara h 1 protein from Arachis hypogea. The Ara h 1 protein has 23 IgE (Immunoglobulin E) binding epitopes, four of which are immunodominant (Y15247, Y15249, Y15250 & Y15263).
                                                                                                                                                                                                                                      593
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                300\ {
m dff} passrdqssylqgfsrntleaafnaefneirrvlleenaggeqeergqrrwstrsse
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                                                                                                                                                                                                                                                                                                                   INAQNNHENFLAGRERNVLQQIEPQAMELAFAASRKEVEELFNSQDESIFFFGPRQHQQQ
                                                                                                                                                                                                                                                                                                                                                                    qqrgrreeeededeeeegsnrevrrytarlkegdvfimpaahpvainasselhll--gfg
                                                                                                                                                                                                                                                                                                                                                                                   RHGGRGGGKRHE-EEEEVHYEQVR---ARLSKREAIVVLAGHPVVFVSSGNENLLLFAFG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    nnegvivkvskehveeltkhaks----vskkgseeegditnpinlregepdlsnnfgkl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     --EGVITRASQEQIRELTRDDSESRRWHIRRGGESSRG----PYNLENKRPLYSNKYGQA 430
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EFFPAGGQNPEPYLSTFSKEILEAALNTQTERLRGVL------
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GGRGALKMIHRDNRESYNLECGDVIRIPAGTTFYLINRDNNERLHIAKFLQTISTPGQYK 335
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      rfstrygnqngrirvlqrfdqrsrqfqnlqnhrivqieakpntlvlpkhadadnilviq
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                                                                                                                                                                                                                                                                                                                                                                                                                                  fevkpdkknpqlqdldmmltcveikegalmlphfnskamvivvvnkgtgnlelvavrkeg
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ksspyqkktenpcagrclqscqqepddlkqk----acesrctkleydprcvydprgh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              626 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative 113;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          to elicit less of an allergic response.
                                                                                   (first entry)
                                                                                                                                                                                                                                      602
                                                                                                                                                                                                                                                                     615
                                                                                                                                                   protein; 626
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           26.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 863.5; DB Pred. No. 1.2e-70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
 class II;
en; fungi;
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 mould; food; ir
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sting;
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                                                                                                                                                                                                                                                                                                                                                                                      В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This invention describes a novel method of desensitizing a patient to a copypeptide allergen and comprises administering to the patient a peptide derived from the allergen where restriction to a MHC Class II molecule possessed by the patient can be demonstrated for the peptide and the copyside is able to induce a late phase response in an individual who possesses the MHC Class II molecule. The methods can be used for copsisting patients to allergens present in e.g. grass, tree and weed (including ragweed) pollens, fungi and moulds, foods, stinging insects, the chiromidae (non-biting midges), spiders and mites, housefly, fruit fly, sheep blow fly, screw worm fly, grain weevil, silkworm, honeybee, non-biting midge larvae, bee moth larvae, mealworm, cockroach, larvae of Tenibrio molitor beetle, mammals such as cat, dog, horse, cow, pig, sheep, rabbit, rat, guinea pig, mice or gerbil. They can also be used to produce immunological vaccines which may be used to prevent and/or treat conditions involving hypersensitivity to allergens. This sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local S
Matches 210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   chiromidae; spider; mite; housefly; fruit fly; sheep blow fly; honeybee screw worm fly; grain weevil; silkworm; bee moth; larvae; mealworm; cat cockroach; beetle; dog; horse; cow; pig; sheep; rabbit; rat; gulnea pig mice; gerbil; vaccine; treatment; prevention; hypersensitivity; peanut
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Desensitizing patients to polypeptide allergens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 1999-458255/38
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         300
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dff pass rdqs sylqgfsrntle aafnae fneir rvlleen aggegeer gqrr ws trsse
                                                                                                                                                                            RSLSTRFRTEEGHISVLENFYGRSKLLRALKNYRLVLLEANPNAFVLPTHLDADAILLVI 275
                                                                                                                                                                                                                                                                                                                                                                              ksspyqkktenpcaqrclqscqqepddlkqk----acesrctkleydprcvydprgh
                                                                                                                                                                                                                                                                                                                                                                                                                      ESDPRQQQY----CQRRCKEICEEEEEYNRQRDPQQQYEQCQKRCQRRETEPR------H 101
                                             EFFPAGGQNPEPYLSTFSKEILEAALNTOTERLRGVL-------GQQR-----
                                                                              qgqatvtvangnnrksfnldeghalripsgfisyilnrhdnqnlrvakismpvntpgqfe 299
                                                                                                                   GGRGALKMIHRDNRESYNLECGDVIRIPAGTTFYLINRDNNERLHIAKFLQTISTPGQYK 335
                                                                                                                                                       rrfstrygnqngrirvlqrfdqrsrqfqnlqnhrivqieakpntlvlpkhadadnilviq 239
                                                                                                                                                                                                                               -dwrqpredw---rrpshqqprkirpegrege----qewgtpgshvreetsrnnpfyfps
                                                                                                                                                                                                                                                                      CEQQEPRLQYQCQRRCQEQQ----RQHGRGGDLMNPQRGGSGRYEEGEEKQSDNPYYFDE
                                                                                                                                                                                                                                                                                                                                           MQICQQRCERRYEKEKRKQQKRYEEQQREDEEKYEERMKEGD - - NKRDPQQREYEDCRRH 159
                                                                                                                                                                                                                                                                                                        tgttnqrsppg-ertrgrqpgdy-----dddrrqprreeggrwgpagprereree----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Page 70-71; 117pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           626 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative 113;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               98GB-0020474
98GB-0000445
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 863.5; DB 20;
Pred. No. 1.2e-70;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 626;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             79;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            fly; honeybee;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       guinea pig;
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This polypeptide comprises major peanut allergen Ara hI (W2214 Its sequence was deduced from cDNA clone P17 (T76612), isolate from peanut seed cDNA using a primer (see T76616) based on an isolated Ara hI peptide (see W24206). The sequence shows significant homology with the vicilin family of seed storage proteins of other legumes. The allergen is recognised by serv
                                                                                                             Peanut allergens Ara hI and Ara hII - used two-site monoclonal antibody based ELISA
                                                                                                                                                                                                                                   04-MAR-1996;
29-DEC-1995;
                                                                                                                                                                                                                                                                                                                                                        Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                       Arachis hypogaea strain Florunner.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Peanut; seed storage protein; allergen; allergy: hypersensitivity; vaccine; anaphylactic shock; immunotherapy; therapy; monoctonal antibody; ELISA; analysis; Ara hI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Peanut allergen Ara
                                                                                                                                                                                                           (UYAR-) UNIV ARKANSAS
                                                                                                                                                                                                                                                                                                                     W09724139-AJ
                                                                                                                                                                                                                                                                                                                                                                                Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   W22149 standard; Protein; 614 AA.
                                                                                                                                                                                                                                                                       23-SEP-1996;
                                                                                                                                                                                                                                                                                              10-JUL-1997.
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DB; T76612.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RHGGRGGGKRHE-EEEEVHYEQVR---ARLSKREAIVVLAGHPVVFVSSGNENLLLFAFG
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                                                                                                                                                                                     GA,
                                                                                      Page 169; 354pp; English.
                                                                                                                                                                                     Burks AW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                                                                                                   96US-0610424
95US-0009455
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                                                                                                                                                                                                                                                                                                                                                                              /label=
23..614
                                                                                                                                                                                                                                                                                                                                                        /label= Mat_protein 521..523
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RESULT W62834

W62834 standard;

Peptide;

614

SON XX DEXX

27-OCT-1998

(first entry)

antimicrobial protein;

infestation; control.

Arachis hypogaea antimicrobial protein

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Best Local S
Matches 220
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                                                                                            VSSGNENLLLFAFGINAQNNHENFLAGRERNVLQQIEPQAMELAFAASRKEVEELFNSQD
                                                                                                                                                                                                                 {\tt epdlsnnfgrlfevkpdkknpqlqdldmmltcveikegalmlphfnskamvivvvnkgtg}
                                                                                                                                                                                                                                                                                                                                                                                         RDPQQREYEDCRRHCEQQEPRLQYQCQRRCQEQQ----RQHGRGGGLMNPQRGGGGRYEE
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eshfvsarpqsqspsspekedqeeenqggkgpllsil
                                                                                                                                                nlelvavrkeqqqrgrreqeweeeeedeeeegsnrevrrytarlkegdvfimpaahpvai
                                                                                                                                                                                    DVEMACPHLSGRHGGRGGGKRHEEEEEVHYE----QVR---ARLSKREAIVVLAGHPVVF
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                                                                                                                                                                                                                                                                                                                                 ---GQQR------EGVIIRASQEQIRELTRDDSESRRWHIRRGGESS--RGPYNLENK 419
                                                                                                                                                                                                                                                                                                                                                                    {\tt akismpvntpgqfedffpassrdqssylqgfsrntleaafnaefneirrvlleenaggeq}
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                                      ESIFFPG-PRQHQQQSPRSTKQQQ-----PLVSIL 620
                                                                       nasselhll--gfginaennhriflagdkdnvidqiekqakdlafpgsgeqvekliknqr
                                                                                                                                                                                                                                                          RPLYSNKYGQAYEVKPEDYR-QLQDMDVSVFIANITQGSMMGPFFNTRSTKVVVVASGEA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CQKRCQRRETEPRHMQICQQRCERRYEKEKRKQQKRYEEQQREDEEKYEERMKEGD--NK 145
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220; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             614 AA;
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%; Pred. No. 2e-70;
1114; Mismatches 205;
   610
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574 eshfvsarpqsqspsspekedqeeenqggkgpllsil 610

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Query Match
Best Local Similarity
Matches 220; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Novel anti-microbial protein from e.g. Macadamia useful for controlling microbial infestations of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 1; Page 55-57; 96pp; English.
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                                                    nasselhll--gfginaennhriflagdkdnvidqiekqakdlafpgsgeqveklikngr 573
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                                                                                    VSSGNENLLLFAFGINAQNNHENFLAGRERNVLQQIEPQAMELAFAASRKEVEELFNSQD 591
                                                                                                                                               nlelvavrkegggrgrregeweeeeedeeeegsnrevrrytarlkegdvfimpaahpvai
                                                                                                                                                                                          DVEMACPHLSGRHGGRGGGKRHEEEEEVHYE----QVR---ARLSKREAIVVLAGHPVVF 531
                                                                                                                                                                                                                                 \verb|epdlsnnfgrlfevkpdkknpqlqdldmmltcveikegalmlphfnskamvivvvnkgtg|\\
                                                                                                                                                                                                                                                                            RPLYSNKYGQAYEVKPEDYR-QLQDMDVSVFIANITQGSMMGPFFNTRSTKVVVVASGEA 478
                                                                                                                                                                                                                                                                                                                                                                                                                                                       AKFLQTISTPGQYKEFFPAGGQNPEPYLSTFSKEILEAALNTQTERLRGVL-----
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                                                                                                                                                                                                                                                                                                                          eergqrrrstrssdnegvivkvskehvqeltkhaksvs----kkgseeeditnpinlrdg
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Best Local S
Matches 203
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Glycine max.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 1; Page 63-65; 96pp; English.
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                                                                                                                                                                                                                                                                                                                                                                            / Match 25.8%; Score 859.5; DB 19; Length Local Similarity 32.1%; Pred. No. 2.7e-70; nes 203; Conservative 133; Mismatches 197; Indels
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                                                                                                                                                                 PQRGGSGRYEEGEEKQ-----SDNPYYFDERSLSTRFRTEEGHISVLENFYGRSKLLRAL 245
                                                                                                                                                                                                                                                              TTFYLINRDNNERLHIAKFLQTISTPGQYKEFFPAGGQNPEPYLSTFSKEILEAALNTQT 365
                                                                                                                                                                                                                          ERLRGVL-----GQQR--EGVIIRASQEQIRELTRDDSESRRWHIRRGGESSRGPY 414
                                                                                            rdyrile fnsk pntlllpnhadadylivilng tailslvnnddrdsyrlqsgdalrvpsg\\
                                                                                                                         KNYRLVLLEANPNAFVLPTHLDADAILLVIGGRGALKMIHRDNRESYNLECGDVIRIPAG
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                                      \verb|ttyyvvnpdnnenlrlitlaipvnkpgrfesfflssteaqqsylqgfsrnileasydtkf|
                                                                                                                                                  -----eesedselrrhknknpflfgsnrfetlfkngygrirvlgrfngrspglgnl 230
                                                                                                                                                                                                                                                                                            QRDPQQQYEQCQKRCQR-----RETEPRHMQICQQRCERRY-EKEKRKQQKRYEEQQRE 130
                                                                                                                                                                                                                                                                                                                      ywekenpkh--nkclqsc-nserdsyrnqacharcnllkvekeeceegeiprprprpqhp 83
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plants or man
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                   This polypeptide comprises major peanut allergen Ara hI (W221 Its sequence was deduced from cDNA clone P41b (T76613), isolated from peanut seed cDNA using a primer (see T76616) based on an isolated Ara hI peptide (see W24206). The sequence shows significant homology with the vicilin family of seed storage proteins of other legumes. The allergen is recognised by sen IgE from a large proportion of individuals with peanut hypersengitivity.
             hypersensitivity
                                                                                                                              Claim 31;
                                                                                                                                                      Peanut allergens Ara hI and Ara hII - used two-site monoclonal antibody based ELISA
                                                                                                                                                                                                        WPI; 1997-363453/33
                                                                                                                                                                                                                                  Bannon GA, Burks AW,
                                                                                                                                                                                                                                                                                      04-MAR-1996;
29-DEC-1995;
                                                                                                                                                                                                                                                                                                                             23-SEP-1996;
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                                                                                                                                                                                                                                                                                                                                                                                                                                               Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Arachis hypogaea strain Florunner.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Peanut; seed storage protein; allergen; allergy; hypersensitivity; vaccine; anaphylactic shock; immunotherapy; therapy; monoclonal antibody; ELISA; analysis; Ara hI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Peanut allergen Ara hI.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            W22150;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Peptide
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                                                                                                                            Page 172;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
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950S-0009455
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521..523
. Ara hI and Ara hII (see antibodies which are used
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Best Local Sim
Matches 209;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MAB ELISA for the detection of Ara hI or Ara hII (claimed). IgE-binding Ara hI antigen epitopes (see W24165-87) may be used in vaccines to protect against allergic reactions to peanut allergens, e.g. anaphylactic shock.
                           Glycine max.
                                                       allergic
                                                                        Peanut; allergen; Ara H 1; IgE; immunoglobulin
                                                                                                                                      06-DEC-1999
                                                                                                                                                                     Y40999
                                                                                                                                                                                                   Y40999 standard;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       YEVKPEDYR-QLQDMDVSVFIANTTQGSMMGPFFNTRSTKVVVVASGEADVEMACPHLSG 489
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 \tt dffpassrdqssylqgfsrntleaafnaefneirrvlleenaggeqeergqrrwstrsse
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MQICQQRCERRYEKEKRKQQKRYEEQQREDEEKYEERMKEGD--NKRDPQQREYEDCRRH 159
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    tgttnqrsppg-ertrgrqpgdy-----dddrrqprreeggrwgpagprereree----
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                                                                                                     beta-conglycinin protein sequence
                                                         reaction;
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                                                                                                                                    (first entry)
                                                                                                                                                                                                   protein;
                                                         soybean; beta-conglycinin.
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Query Match
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Matches 203
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Disclosure; Fig 33A-B; 193pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Tertiary structure of peanut allergen Ara animal from allergic reaction - \,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       12-MAR-1998;
11-MAR-1999;
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es 203; Conserv
                                                                                                                                                                                                                                          IRIPAGTTFYLINRDNWERLHIAKFLQTISTPGQYKEFFPAGGQNPEPYLSTFSKEILEA 359
                                                                                                                                ALNTQTERLRGVL-----GQOR--EGVIIRASQEQIRELTRDDSESRRWHIRRGGE 408
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KVVVVASGEADVEMACPHLSGRHGGRGGGKRHEEEEEEVHYEQ-----VRARLSKREAIV 522
                                      KLLRALKNYRLVLLEANPNAFVLPTHLDADAILLVIGGRGALKMIHRDNRESYNLECGDV 299
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                                                                                     SSRGPYNLFNKRPLYSNKYGQAYEVKPEDYRQLQDMDVSVFIANITQGSMMGPFFNTRST 468
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -rprpqhperep-----qqpgekeededeqprpipfprpqprqeeeheqreeqewprke 129
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